

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/22 19:48:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617654.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR8617654 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617654_1.fastq.gz SRR8617654_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Dec 22 19:48:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617654.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,509,750
Mapped reads	2,480,339 / 98.83%
Unmapped reads	29,411 / 1.17%
Mapped paired reads	2,480,339 / 98.83%
Mapped reads, first in pair	1,242,005 / 49.49%
Mapped reads, second in pair	1,238,334 / 49.34%
Mapped reads, both in pair	2,472,608 / 98.52%
Mapped reads, singletons	7,731 / 0.31%
Secondary alignments	0
Supplementary alignments	27,491 / 1.1%
Read min/max/mean length	30 / 151 / 151.53
Duplicated reads (estimated)	377,894 / 15.06%
Duplication rate	14.97%
Clipped reads	1,802,516 / 71.82%

2.2. ACGT Content

Number/percentage of A's	97,657,503 / 29.2%
Number/percentage of C's	67,834,277 / 20.28%
Number/percentage of T's	97,337,600 / 29.11%
Number/percentage of G's	71,566,872 / 21.4%
Number/percentage of N's	20,895 / 0.01%

GC Percentage	41.68%
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2.3. Coverage

Mean	0.1081
Standard Deviation	1.1989

2.4. Mapping Quality

Mean Mapping Quality	53.73
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2.5. Insert size

Mean	78,332.82
Standard Deviation	2,693,377.08
P25/Median/P75	136 / 169 / 213

2.6. Mismatches and indels

General error rate	1.07%
Mismatches	3,434,984
Insertions	66,234
Mapped reads with at least one insertion	2.55%
Deletions	128,485
Mapped reads with at least one deletion	4.99%
Homopolymer indels	46.64%

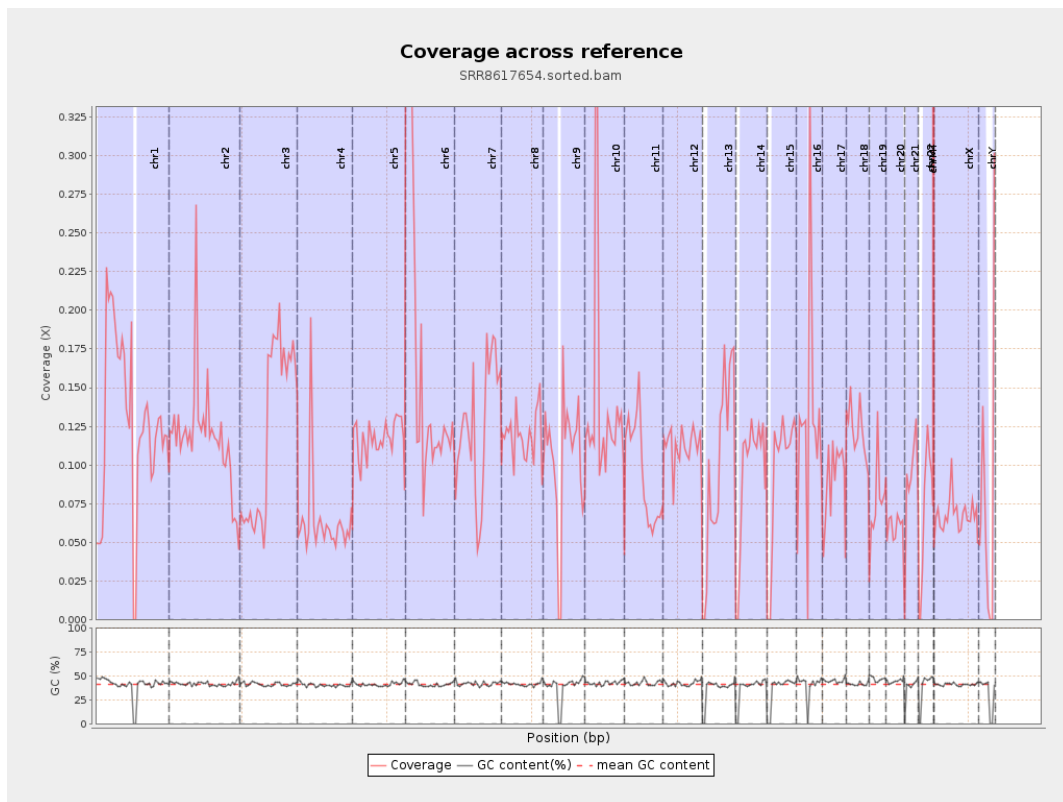
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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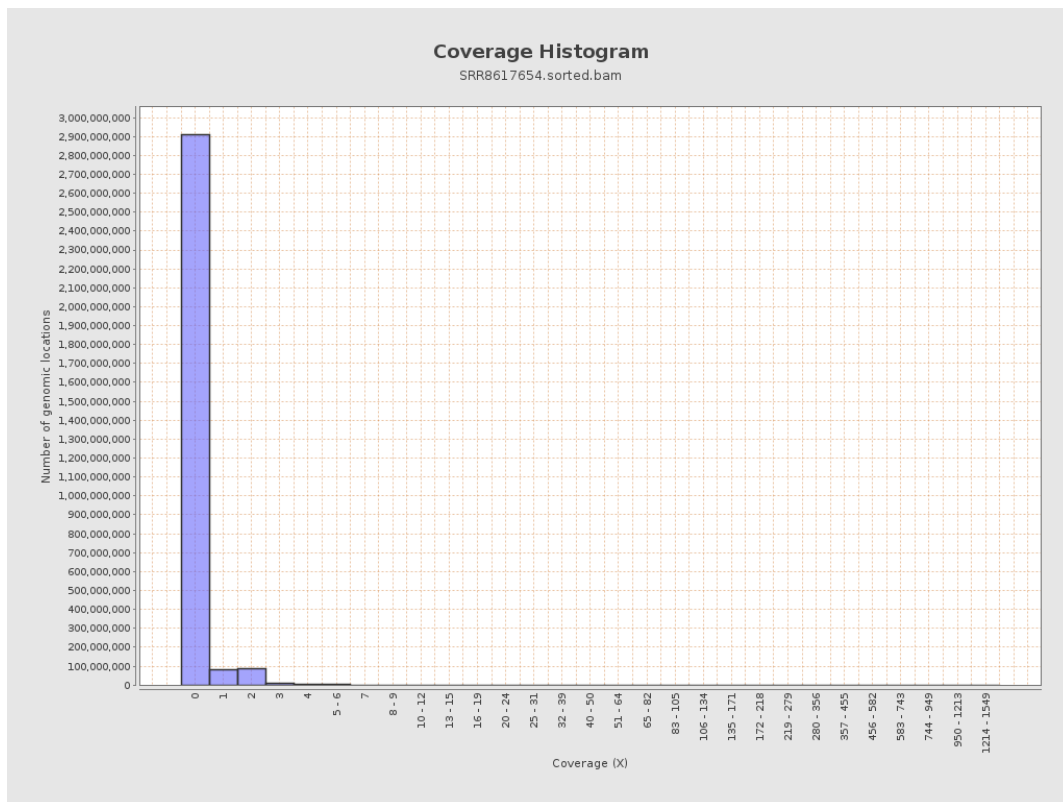
		bases	coverage	deviation
chr1	249250621	31848231	0.1278	1.3818
chr2	243199373	28673476	0.1179	1.1874
chr3	198022430	23905948	0.1207	0.5101
chr4	191154276	11985560	0.0627	0.7753
chr5	180915260	21117669	0.1167	0.4838
chr6	171115067	27763451	0.1623	1.0184
chr7	159138663	19928725	0.1252	1.3099
chr8	146364022	17465895	0.1193	0.5881
chr9	141213431	14675500	0.1039	1.7146
chr10	135534747	18772331	0.1385	3.1801
chr11	135006516	12530099	0.0928	1.2531
chr12	133851895	14946380	0.1117	0.4701
chr13	115169878	11499704	0.0998	0.4478
chr14	107349540	10146424	0.0945	0.4448
chr15	102531392	9885399	0.0964	0.4374
chr16	90354753	11418841	0.1264	1.637
chr17	81195210	7206265	0.0888	1.0082
chr18	78077248	9567914	0.1225	1.583
chr19	59128983	4592424	0.0777	0.8467
chr20	63025520	3710066	0.0589	0.4074
chr21	48129895	4314896	0.0897	0.6248
chr22	51304566	3575206	0.0697	0.3782
chrMT	16571	73270	4.4216	3.5533
chrX	155270560	10502281	0.0676	0.5196

chrY	59373566	4554583	0.0767	1.7684
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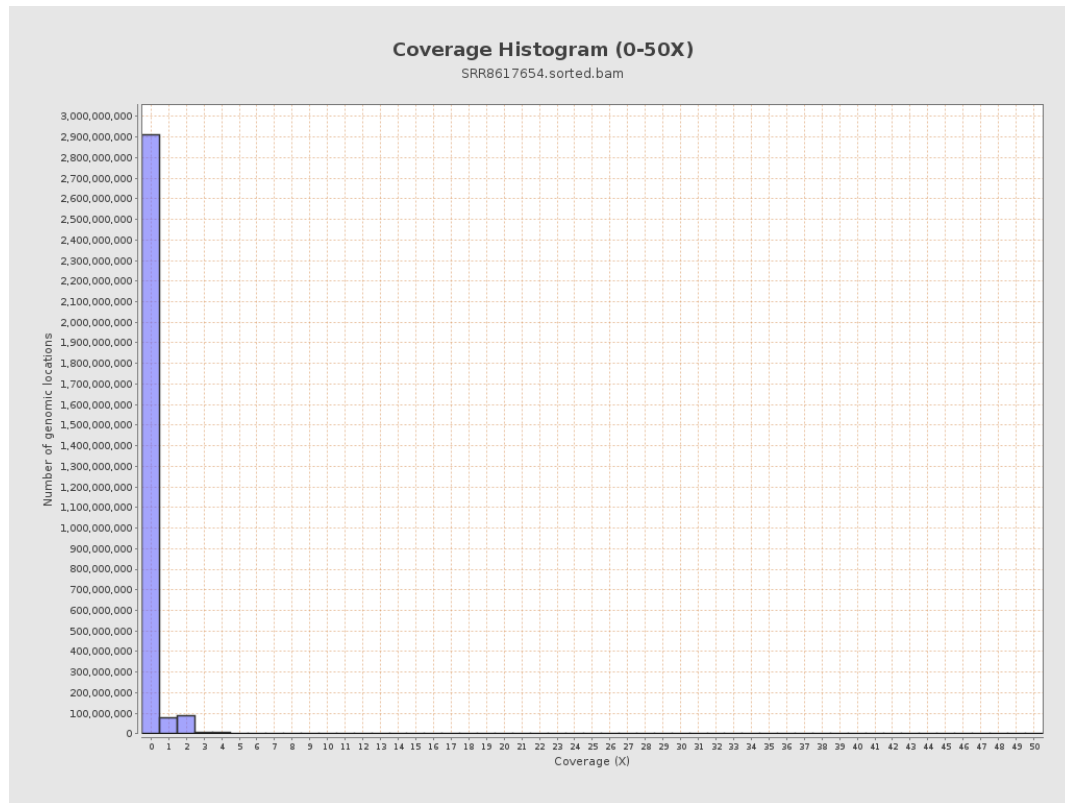
3. Results : Coverage across reference



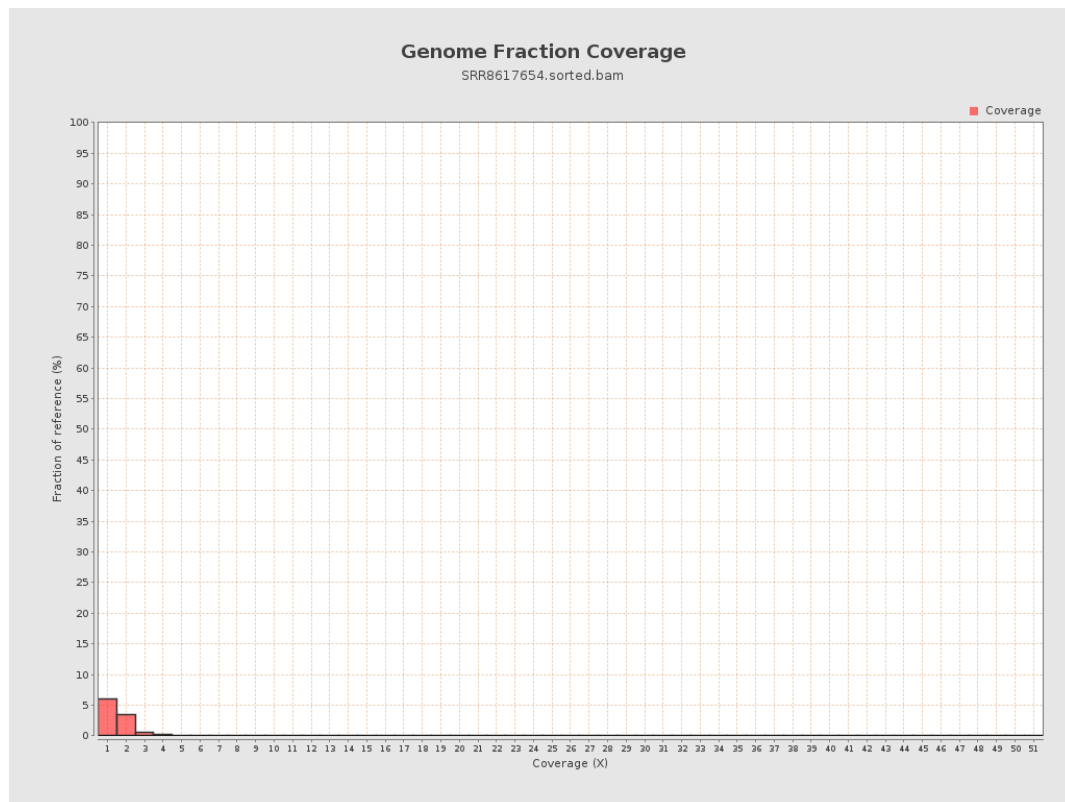
4. Results : Coverage Histogram



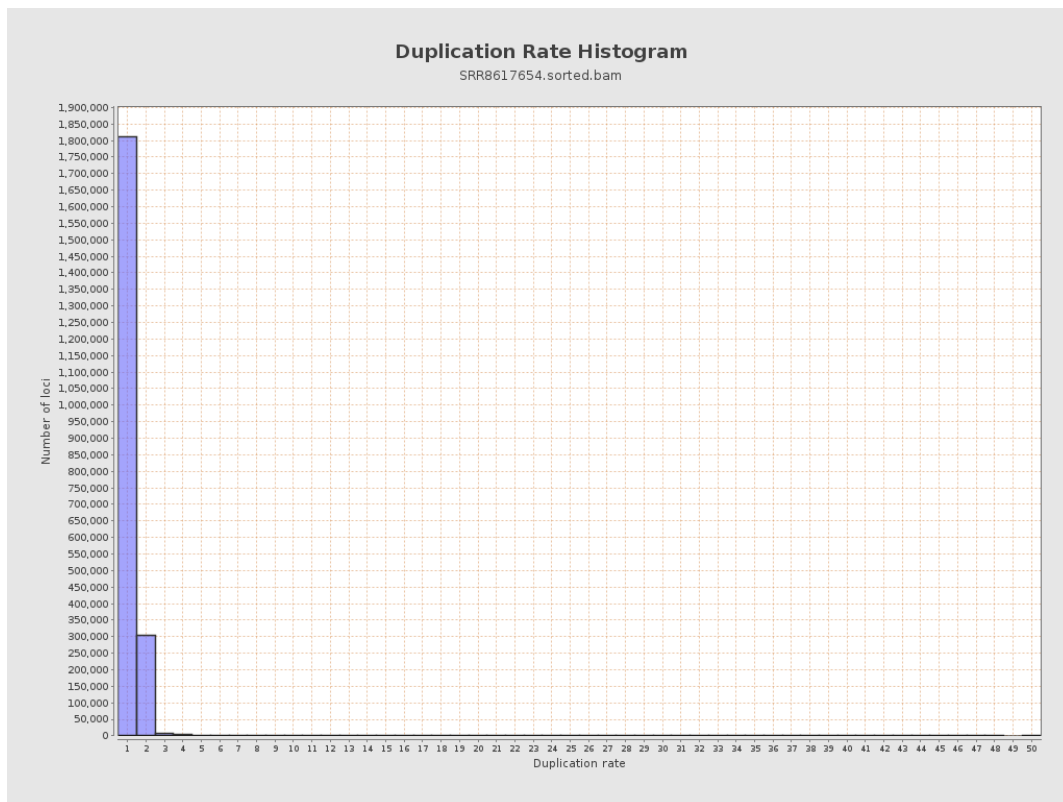
5. Results : Coverage Histogram (0-50X)



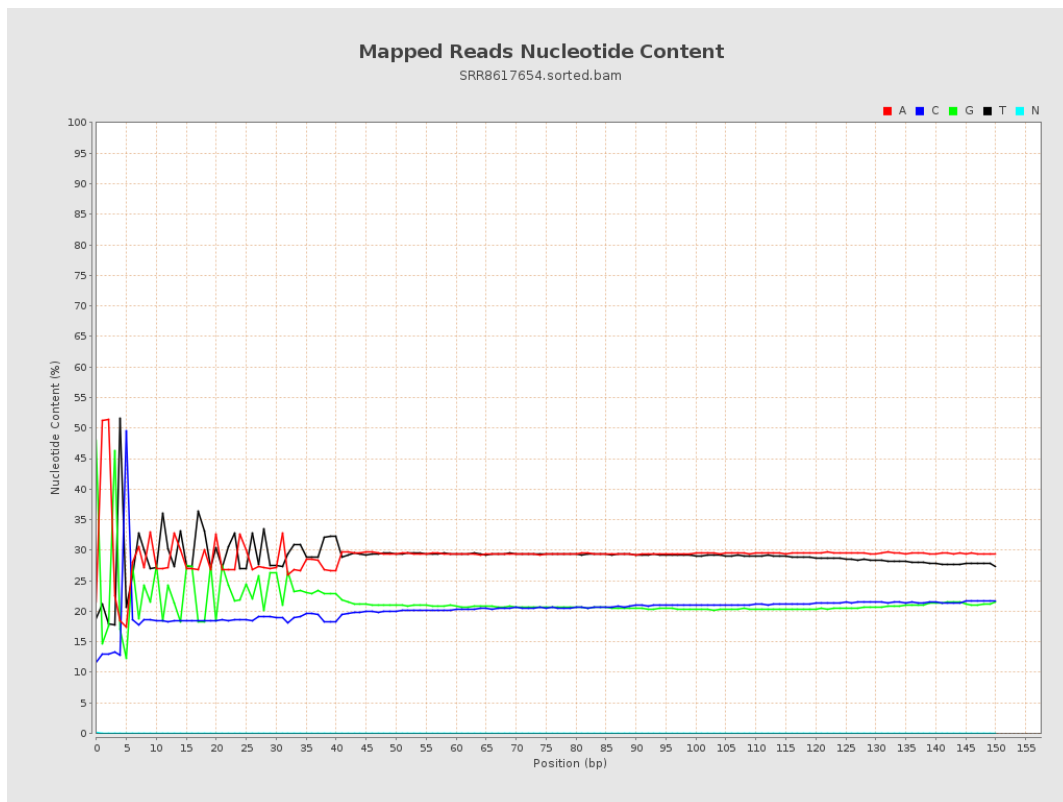
6. Results : Genome Fraction Coverage



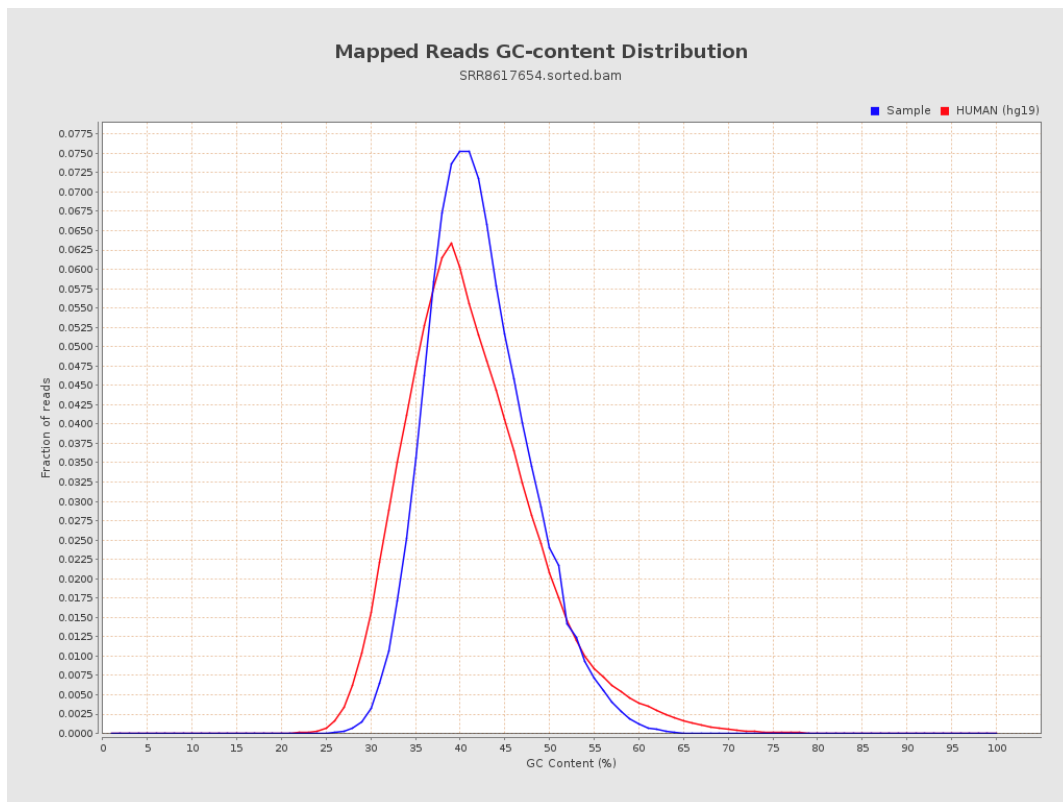
7. Results : Duplication Rate Histogram



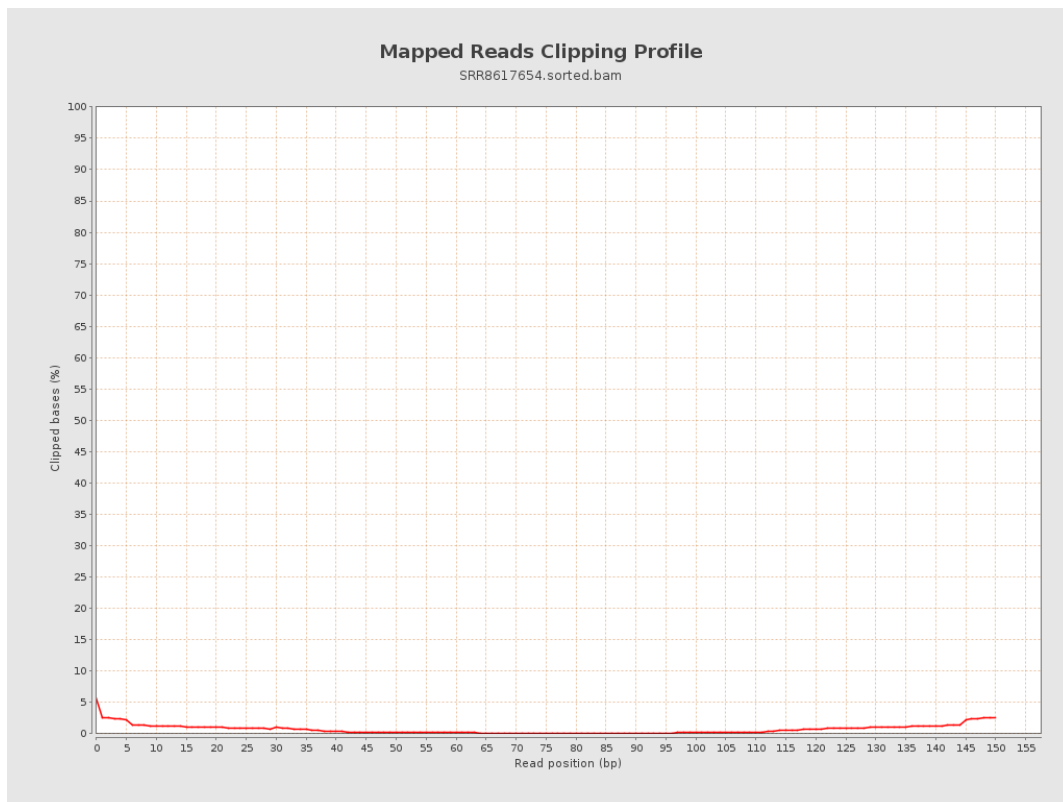
8. Results : Mapped Reads Nucleotide Content



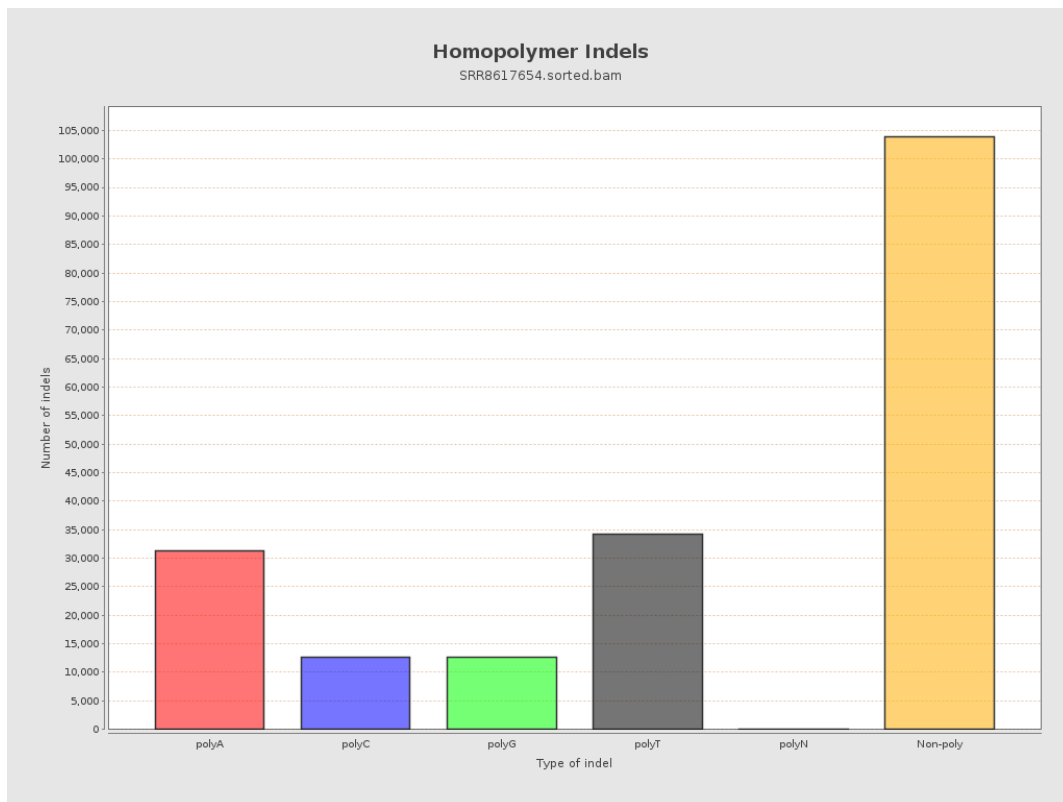
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



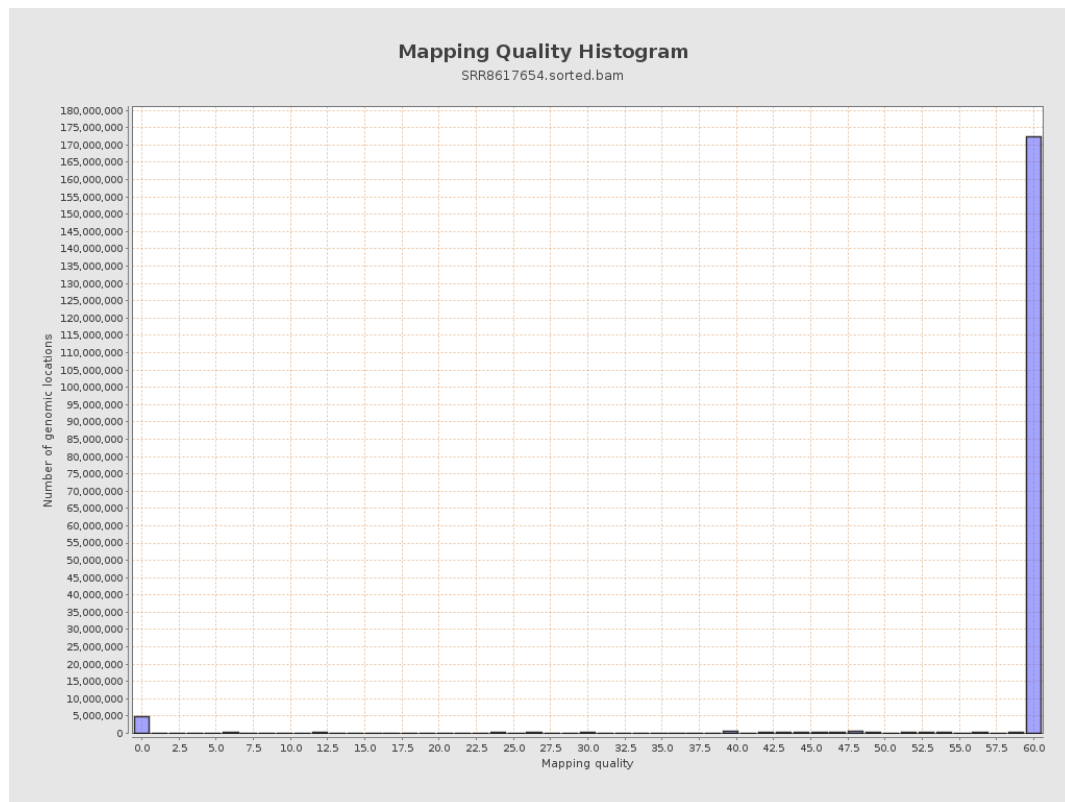
11. Results : Homopolymer Indels



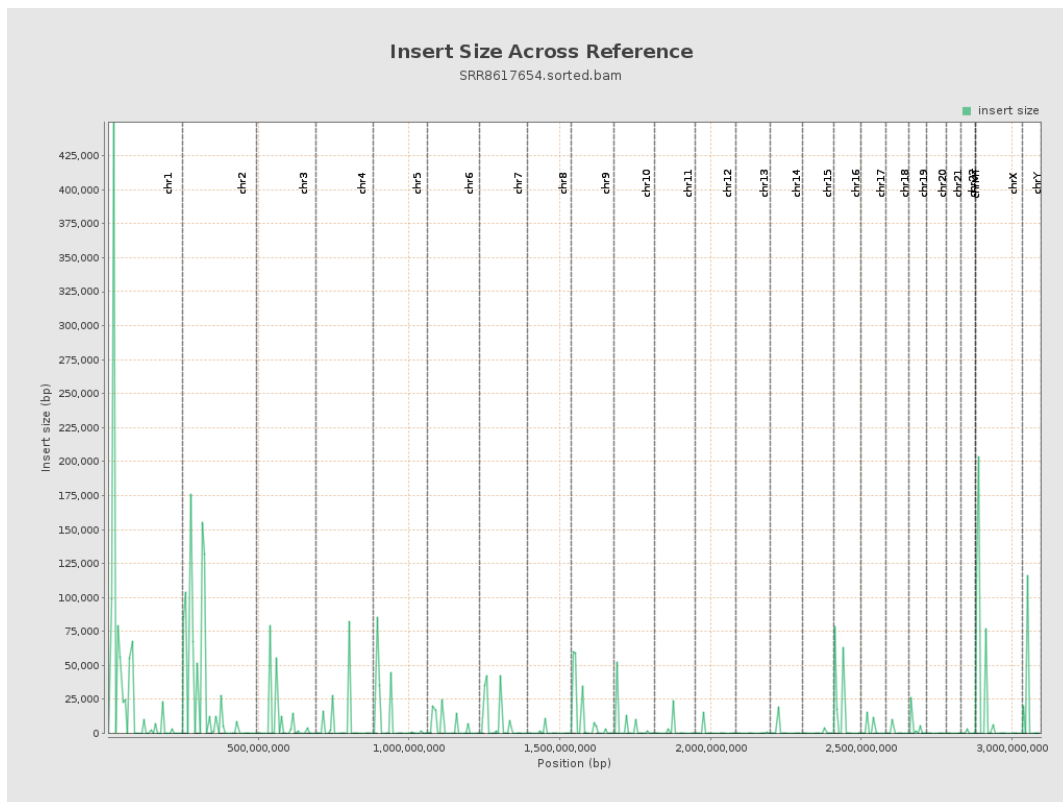
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

